



SEQUENCE LISTING

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GROS, PHILIPPE
DUBOW, MICHAEL

<120> COMPOSITIONS AND METHODS INVOLVING AN ESSENTIAL
STAPHYLOCOCCUS AUREUS GENE AND ITS ENCODED PROTEIN
STAAU_R9

<130> 073406-0701

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<150> 60/256,349

<151> 2000-12-19

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 1800

<212> DNA

<213> Staphylococcus aureus

<400> 1

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catgatgaaa agacaccttc atttacagtt tctgaagata aacaaatttg tcattgtttt 180
ggttgtaaaa aaggtggcaa tgtttttcaa tttactcaag aaattaaaga catatcattt 240
gttgaagcgg ttaaagaatt aggtgataga gttaatgttg ctgtagatat tgaggcaaca 300
caatctaact caaatgttca aattgcttct gatgatttac aaatgattga aatgcatgag 360
ttaatacaag aattttatta ttacgcttta acaagacag tcgaaggcga acaagcatta 420
acgtacttac aagaacgtgg ttttacagat gcgcttatta aagagcgagg cattggcttt 480
gcacccgata gctcacattt ttgtcatgat tttcttcaaa aaaagggtta cgatattgaa 540
ttagcatatg aagccggatt attatcacgt aacgaagaaa atttcagtta ttacgataga 600
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caaaaaagaa agttgttata caacttagat aaagcgcgta aatcaattag aaaattagat 780
gaaatcgtat tactagaagg ttttatggat gttataaaat ctgatactgc tggcttgaaa 840
aacgttggtg caacaatggg tacacagttg tcagatgaac atattacttt tatacgaaag 900
ttaacatcaa atataacatt aatgtttgat ggggattttg cgggtagtga agcaacactt 960
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aaaaatgaca aaaagtcatt tgcacattat aaagtgagta tattaaaaga tgaaattgca 1140
cataatgacc tttcatatga acgttatattg aaagaactaa gtcatgatat ttcgcttatg 1200
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cctgagcaat tagctaacga aatacaattc aatcaagcac cagccaatta ttatccagaa 1320
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gtgcagtatg ttaattcaaa tgagttgaga gaaacactaa ttagctttaga acaatataat 1620
ttgaatgacg aaccatagta aatgaaatt gatgattatg tcaatgttat taatgaaaaa 1680
ggacaagaaa caattgagtc attgaatcat aaattaaggg aagctacaag gattggcgat 1740
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<210> 2
 <211> 599
 <212> PRT
 <213> Staphylococcus aureus

<400> 2

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		20						25					30		
Asn	Tyr	Ile	Gly	Leu	Cys	Pro	Phe	His	Asp	Glu	Lys	Thr	Pro	Ser	Phe
		35					40					45			
Thr	Val	Ser	Glu	Asp	Lys	Gln	Ile	Cys	His	Cys	Phe	Gly	Cys	Lys	Lys
	50					55					60				
Gly	Gly	Asn	Val	Phe	Gln	Phe	Thr	Gln	Glu	Ile	Lys	Asp	Ile	Ser	Phe
65					70					75					80
Val	Glu	Ala	Val	Lys	Glu	Leu	Gly	Asp	Arg	Val	Asn	Val	Ala	Val	Asp
			85						90						95
Ile	Glu	Ala	Thr	Gln	Ser	Asn	Ser	Asn	Val	Gln	Ile	Ala	Ser	Asp	Asp
			100					105						110	
Leu	Gln	Met	Ile	Glu	Met	His	Glu	Leu	Ile	Gln	Glu	Phe	Tyr	Tyr	Tyr
		115					120					125			
Ala	Leu	Thr	Lys	Thr	Val	Glu	Gly	Glu	Gln	Ala	Leu	Thr	Tyr	Leu	Gln
	130					135					140				
Glu	Arg	Gly	Phe	Thr	Asp	Ala	Leu	Ile	Lys	Glu	Arg	Gly	Ile	Gly	Phe
145					150					155					160
Ala	Pro	Asp	Ser	Ser	His	Phe	Cys	His	Asp	Phe	Leu	Gln	Lys	Lys	Gly
			165						170					175	
Tyr	Asp	Ile	Glu	Leu	Ala	Tyr	Glu	Ala	Gly	Leu	Leu	Ser	Arg	Asn	Glu
		180						185					190		
Glu	Asn	Phe	Ser	Tyr	Tyr	Asp	Arg	Phe	Arg	Asn	Arg	Ile	Met	Phe	Pro
	195						200					205			
Leu	Lys	Asn	Ala	Gln	Gly	Arg	Ile	Val	Gly	Tyr	Ser	Gly	Arg	Thr	Tyr
	210					215					220				
Thr	Gly	Gln	Glu	Pro	Lys	Tyr	Leu	Asn	Ser	Pro	Glu	Thr	Pro	Ile	Phe
225					230					235					240
Gln	Lys	Arg	Lys	Leu	Leu	Tyr	Asn	Leu	Asp	Lys	Ala	Arg	Lys	Ser	Ile
			245						250					255	
Arg	Lys	Leu	Asp	Glu	Ile	Val	Leu	Leu	Glu	Gly	Phe	Met	Asp	Val	Ile
		260						265					270		

Lys Ser Asp Thr Ala Gly Leu Lys Asn Val Val Ala Thr Met Gly Thr
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 Gln Leu Ser Asp Glu His Ile Thr Phe Ile Arg Lys Leu Thr Ser Asn
 290 295 300
 Ile Thr Leu Met Phe Asp Gly Asp Phe Ala Gly Ser Glu Ala Thr Leu
 305 310 315 320
 Lys Thr Gly Gln Asn Leu Leu Gln Gln Gly Leu Asn Val Phe Val Ile
 325 330 335
 Gln Leu Pro Ser Gly Met Asp Pro Asp Glu Tyr Ile Gly Lys Tyr Gly
 340 345 350
 Asn Asp Ala Phe Thr Ala Phe Val Lys Asn Asp Lys Lys Ser Phe Ala
 355 360 365
 His Tyr Lys Val Ser Ile Leu Lys Asp Glu Ile Ala His Asn Asp Leu
 370 375 380
 Ser Tyr Glu Arg Tyr Leu Lys Glu Leu Ser His Asp Ile Ser Leu Met
 385 390 395 400
 Lys Ser Ser Ile Leu Gln Gln Lys Ala Leu Asn Asp Val Ala Pro Phe
 405 410 415
 Phe Asn Val Ser Pro Glu Gln Leu Ala Asn Glu Ile Gln Phe Asn Gln
 420 425 430
 Ala Pro Ala Asn Tyr Tyr Pro Glu Asp Glu Tyr Gly Gly Tyr Ile Glu
 435 440 445
 Pro Glu Pro Ile Gly Met Ala Gln Phe Asp Asn Leu Ser Arg Gln Glu
 450 455 460
 Lys Ala Glu Arg Ala Phe Leu Lys His Leu Met Arg Asp Lys Asp Thr
 465 470 475 480
 Phe Leu Asn Tyr Tyr Glu Ser Val Asp Lys Asp Asn Phe Thr Asn Gln
 485 490 495
 His Phe Lys Tyr Val Phe Glu Val Leu His Asp Phe Tyr Ala Glu Asn
 500 505 510
 Asp Gln Tyr Asn Ile Ser Asp Ala Val Gln Tyr Val Asn Ser Asn Glu
 515 520 525
 Leu Arg Glu Thr Leu Ile Ser Leu Glu Gln Tyr Asn Leu Asn Asp Glu
 530 535 540
 Pro Tyr Glu Asn Glu Ile Asp Asp Tyr Val Asn Val Ile Asn Glu Lys
 545 550 555 560
 Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys Leu Arg Glu Ala Thr
 565 570 575

Arg Ile Gly Asp Val Glu Leu Gln Lys Tyr Tyr Leu Gln Gln Ile Val
 580 585 590

Ala Lys Asn Lys Glu Arg Met
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<210> 3
 <211> 216
 <212> DNA
 <213> Staphylococcus aureus

<400> 3
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 aataacgagt tatcgctttt cgatgattac gacagagttg aaaagaaaat catgaatgaa 180
 atcaactgga agaaaacaca cattaaggag tgttaa 216

<210> 4
 <211> 71
 <212> PRT
 <213> Staphylococcus aureus

<400> 4
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Thr Lys Gln Ser Asp Pro Ile Val Ala Asn Val Tyr Ile Glu Thr Gly
 20 25 30

Trp Ala Val Asn Arg Leu Leu Asp Asn Asn Glu Leu Ser Pro Phe Asp
 35 40 45

Asp Tyr Asp Arg Val Glu Lys Lys Ile Met Asn Glu Ile Asn Trp Lys
 50 55 60

Lys Thr His Ile Lys Glu Cys
 65 70

<210> 5
 <211> 120
 <212> DNA
 <213> Staphylococcus aureus

<400> 5
 ggacaagaaa caattgagtc attgaatcat aaattaaggg aagctacaag gattggcgat 60
 gtagaattac aaaaatacta ttacagcaa attgttgcta agaataaaga acgcatgtag 120

<210> 6
 <211> 39
 <212> PRT
 <213> Staphylococcus aureus

<400> 6

Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys Leu Arg Glu Ala Thr
 1 5 10 15

Arg Ile Gly Asp Val Glu Leu Gln Lys Tyr Tyr Leu Gln Gln Ile Val
 20 25 30

Ala Lys Asn Lys Glu Arg Met
 35

<210> 7

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 7

cgcggtatccc tatccttttt cattaataac attg

34

<210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 8

ccggaattct tgcgaataga tcaatcg

27

<210> 9

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

ggaagatctc tacatgcgtt ctttatcc

28

<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

ccggaattca tgataggttt gtgtcct

27

<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ccggaattcc caaaatacct aaatagtcc

29

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
ccggaattcg cacataatga cctttca

27

<210> 13
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
cgcggatcca tgcctgatgg caattg

26

<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
ccatcgatga tttcataagc gaaatatc

28

<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
ccggaattcc ctgagccaat tggatatggc

29

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
cgcggatccc taagggtcaa tgtaaccgcc

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<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
ccggaattca aggataactt cacaaatcag

30

<210> 18
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
cgcggatccc tacttatcaa cactttcata ata

33

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
ccggaattca gagaaacact aattagctta

30

<210> 20
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 20

cgcggatccc tatctcaact catttgaatt aac

33

<210> 21

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 21

ccggaattcg gacaagaaac aattgagtc

29

<210> 22

<211> 581

<212> PRT

<213> Escherichia coli

<400> 22

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Thr	Asp	Ile	Val	Asp	Leu	Ile	Asp	Ala	Arg	Val	Lys	Leu	Lys	Lys	Gln
		20						25					30		

Gly	Lys	Asn	Phe	His	Ala	Cys	Cys	Pro	Phe	His	Asn	Glu	Lys	Thr	Pro
	35						40					45			

Ser	Phe	Thr	Val	Asn	Gly	Glu	Lys	Gln	Phe	Tyr	His	Cys	Phe	Gly	Cys
	50					55					60				

Gly	Ala	His	Gly	Asn	Ala	Ile	Asp	Phe	Leu	Met	Asn	Tyr	Asp	Lys	Leu
65					70					75					80

Glu	Phe	Val	Glu	Thr	Val	Glu	Glu	Leu	Ala	Ala	Met	His	Asn	Leu	Glu
			85					90						95	

Val	Pro	Phe	Glu	Ala	Gly	Ser	Gly	Pro	Ser	Gln	Ile	Glu	Arg	His	Gln
		100						105					110		

Arg	Gln	Thr	Leu	Tyr	Gln	Leu	Met	Asp	Gly	Leu	Asn	Thr	Phe	Tyr	Gln
	115						120					125			

Gln	Ser	Leu	Gln	Gln	Pro	Val	Ala	Thr	Ser	Ala	Arg	Gln	Tyr	Leu	Glu
	130					135					140				

Lys	Arg	Gly	Leu	Ser	His	Glu	Val	Ile	Ala	Arg	Phe	Ala	Ile	Gly	Phe
145					150					155				160	

Ala	Pro	Pro	Gly	Trp	Asp	Asn	Val	Leu	Lys	Arg	Phe	Gly	Gly	Asn	Pro
				165					170					175	

Glu Asn Arg Gln Ser Leu Ile Asp Ala Gly Met Leu Val Thr Asn Asp
 180 185 190
 Gln Gly Arg Ser Tyr Asp Arg Phe Arg Glu Arg Val Met Phe Pro Ile
 195 200 205
 Arg Asp Lys Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Val Leu Gly
 210 215 220
 Asn Asp Thr Pro Lys Tyr Leu Asn Ser Pro Glu Thr Asp Ile Phe His
 225 230 235 240
 Lys Gly Arg Gln Leu Tyr Gly Leu Tyr Glu Ala Gln Gln Asp Asn Ala
 245 250 255
 Glu Pro Asn Arg Leu Leu Val Val Glu Gly Tyr Met Asp Val Val Ala
 260 265 270
 Leu Ala Gln Tyr Gly Ile Asn Tyr Ala Val Ala Ser Leu Gly Thr Ser
 275 280 285
 Thr Thr Ala Asp His Ile Gln Leu Leu Phe Arg Ala Thr Asn Asn Val
 290 295 300
 Ile Cys Cys Tyr Asp Gly Asp Arg Ala Gly Arg Asp Ala Ala Trp Arg
 305 310 315 320
 Ala Leu Glu Thr Ala Leu Pro Tyr Met Thr Asp Gly Arg Gln Leu Arg
 325 330 335
 Phe Met Phe Leu Pro Asp Gly Glu Asp Pro Asp Thr Leu Val Arg Lys
 340 345 350
 Glu Gly Lys Glu Ala Phe Glu Ala Arg Met Glu Gln Ala Met Pro Leu
 355 360 365
 Ser Ala Phe Leu Phe Asn Ser Leu Met Pro Gln Val Asp Leu Ser Thr
 370 375 380
 Pro Asp Gly Arg Ala Arg Leu Ser Thr Leu Ala Leu Pro Leu Ile Ser
 385 390 395 400
 Gln Val Pro Gly Glu Thr Leu Arg Ile Tyr Leu Arg Gln Glu Leu Gly
 405 410 415
 Asn Lys Leu Gly Ile Leu Asp Asp Ser Gln Leu Glu Arg Leu Met Pro
 420 425 430
 Lys Ala Ala Glu Ser Gly Val Ser Arg Pro Val Pro Gln Leu Lys Arg
 435 440 445
 Thr Thr Met Arg Ile Leu Ile Gly Leu Leu Val Gln Asn Pro Glu Leu
 450 455 460
 Ala Thr Leu Val Pro Pro Leu Glu Asn Leu Asp Glu Asn Lys Leu Pro
 465 470 475 480

Gly Leu Gly Leu Phe Arg Glu Leu Val Asn Thr Cys Leu Ser Gln Pro
 485 490 495

Gly Leu Thr Thr Gly Gln Leu Leu Glu His Tyr Arg Gly Thr Asn Asn
 500 505 510

Ala Ala Thr Leu Glu Lys Leu Ser Met Trp Asp Asp Ile Ala Asp Lys
 515 520 525

Asn Ile Ala Glu Gln Thr Phe Thr Asp Ser Leu Asn His Met Phe Asp
 530 535 540

Ser Leu Leu Glu Leu Arg Gln Glu Glu Leu Ile Ala Arg Glu Arg Thr
 545 550 555 560

His Gly Leu Ser Asn Glu Glu Arg Leu Glu Leu Trp Thr Leu Asn Gln
 565 570 575

Glu Leu Ala Lys Lys
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<210> 23

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 23

ccgctcgagc tccaaattcc aaaacag

27

<210> 24

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24

cgggatccaa taagactcct ttttac

26

<210> 25

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 25

gcgcactctgt aaaaccacg

19

<210> 26
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 26
 gcacgaattc aagaagaatt g

21

<210> 27
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 27
 gatctcgtcg tgcattctgtt ggatccccgg aattccccggg

40

<210> 28
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 28
 tcgacccggg aattccgggg atccaacaga tgcacgacga

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<210> 29
 <211> 9
 <212> PRT
 <213> Staphylococcus aureus

<400> 29
 Tyr Tyr Leu Gln Gln Ile Val Ala Lys
 1 5

<210> 30
 <211> 10
 <212> PRT
 <213> Staphylococcus aureus

<400> 30
 Glu Leu Ser His Asp Ile Ser Leu Met Lys
 1 5 10

<210> 31
 <211> 10
 <212> PRT
 <213> Staphylococcus aureus

<400> 31
 Ile Asp Gln Ser Ile Ile Asn Glu Ile Lys
 1 5 10

<210> 32
 <211> 11
 <212> PRT
 <213> Staphylococcus aureus

<400> 32
 Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys
 1 5 10

<210> 33
 <211> 10
 <212> PRT
 <213> Staphylococcus aureus

<400> 33
 Asn Glu Glu Asn Phe Ser Tyr Tyr Asp Arg
 1 5 10

<210> 34
 <211> 12
 <212> PRT
 <213> Staphylococcus aureus

<400> 34
 Tyr Leu Asn Ser Pro Glu Thr Pro Ile Phe Gln Lys
 1 5 10

<210> 35
 <211> 16
 <212> PRT
 <213> Staphylococcus aureus

<400> 35
 Lys Gly Tyr Asp Ile Glu Leu Ala Tyr Glu Ala Gly Leu Leu Ser Arg
 1 5 10 15

<210> 36
 <211> 17
 <212> PRT
 <213> Staphylococcus aureus

<400> 36
 Val Ser Ile Leu Lys Asp Glu Ile Ala His Asn Asp Leu Ser Tyr Glu
 1 5 10 15

Arg

<210> 37

<211> 98

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Illustrative
zf-CHC2 comparison peptide

<400> 37

Ile	Pro	Glu	Glu	Ser	Ile	Asp	Glu	Leu	Lys	Asn	Arg	Ile	Asp	Ile	Val
1				5					10					15	

Asp	Val	Ile	Ser	Glu	Tyr	Val	Lys	Leu	Lys	Lys	Lys	Gly	Arg	Asn	Tyr
			20					25					30		

Lys	Gly	Leu	Cys	Pro	Phe	His	Asp	Glu	Lys	Thr	Pro	Ser	Phe	Ser	Val
		35					40					45			

Ser	Pro	Glu	Lys	Gln	Phe	Tyr	His	Cys	Phe	Gly	Cys	Gly	Ala	Gly	Gly
	50					55					60				

Asp	Ala	Ile	Lys	Phe	Leu	Met	Lys	Tyr	Glu	Lys	Leu	Ser	Phe	Val	Glu
65					70					75					80

Ala	Val	Glu	Lys	Leu	Ala	Asp	Arg	Ala	Gly	Ile	Asp	Leu	Pro	Tyr	Glu
			85						90					95	

Lys Gly

<210> 38

<211> 151

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Illustrative
toprim comparison peptide

<400> 38

Lys	Val	Leu	Ile	Ile	Val	Glu	Gly	Pro	Ser	Asp	Ala	Lys	Ala	Leu	Ala
1				5					10					15	

Lys	Ala	Leu	Gly	Lys	Pro	Ser	Lys	Arg	Lys	Ile	Val	Tyr	Glu	Leu	Pro
		20					25						30		

Gly	Gly	Lys	Asp	Gly	Asn	Val	Val	Ala	Ser	Leu	Gly	His	Leu	Val	Asp
		35				40						45			

Leu	Pro	Thr	Pro	Glu	Gly	Tyr	Asp	Asp	Lys	Tyr	Lys	Trp	Leu	Trp	Leu
	50					55					60				

Pro Ile Val Asp Val Lys Lys Gly Phe Glu Pro Tyr Gln Ile Glu Phe
65 70 75 80

Asp Gln Leu Cys Lys Cys Ser Lys Lys Ile Asp Leu Lys Lys Glu Gln
85 90 95

Leu Lys Leu Leu Lys Lys Leu Ala Lys Lys Ala Asp Glu Val Ile Leu
100 105 110

Ala Thr Asp Pro Asp Arg Glu Gly Glu Ala Ile Ala Trp Lys Leu Leu
115 120 125

Glu Leu Leu Lys Pro Tyr Gly Pro Val Glu Leu Glu Asp Asp Lys Lys
130 135 140

Val Arg Arg Ile Phe Leu Pro
145 150

<210> 39

<211> 572

<212> PRT

<213> Staphylococcus aureus

<400> 39

Met Ile Gly Leu Cys Pro Phe His Asp Glu Lys Thr Pro Ser Phe Thr
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Val Ser Glu Asp Lys Gln Ile Cys His Cys Phe Gly Cys Lys Lys Gly
20 25 30

Gly Asn Val Phe Gln Phe Thr Gln Glu Ile Lys Asp Ile Ser Phe Val
35 40 45

Glu Ala Val Lys Glu Leu Gly Asp Arg Val Asn Val Ala Val Asp Ile
50 55 60

Glu Ala Thr Gln Ser Asn Ser Asn Val Gln Ile Ala Ser Asp Asp Leu
65 70 75 80

Gln Met Ile Glu Met His Glu Leu Ile Gln Glu Phe Tyr Tyr Tyr Ala
85 90 95

Leu Thr Lys Thr Val Glu Gly Glu Gln Ala Leu Thr Tyr Leu Gln Glu
100 105 110

Arg Gly Phe Thr Asp Ala Leu Ile Lys Glu Arg Gly Ile Gly Phe Ala
115 120 125

Pro Asp Ser Ser His Phe Cys His Asp Phe Leu Gln Lys Lys Gly Tyr
130 135 140

Asp Ile Glu Leu Ala Tyr Glu Ala Gly Leu Leu Ser Arg Asn Glu Glu
145 150 155 160

Asn Phe Ser Tyr Tyr Asp Arg Phe Arg Asn Arg Ile Met Phe Pro Leu
165 170 175

Lys Asn Ala Gln Gly Arg Ile Val Gly Tyr Ser Gly Arg Thr Tyr Thr
 180 185 190
 Gly Gln Glu Pro Lys Tyr Leu Asn Ser Pro Glu Thr Pro Ile Phe Gln
 195 200 205
 Lys Arg Lys Leu Leu Tyr Asn Leu Asp Lys Ala Arg Lys Ser Ile Arg
 210 215 220
 Lys Leu Asp Glu Ile Val Leu Leu Glu Gly Phe Met Asp Val Ile Lys
 225 230 235 240
 Ser Asp Thr Ala Gly Leu Lys Asn Val Val Ala Thr Met Gly Thr Gln
 245 250 255
 Leu Ser Asp Glu His Ile Thr Phe Ile Arg Lys Leu Thr Ser Asn Ile
 260 265 270
 Thr Leu Met Phe Asp Gly Asp Phe Ala Gly Ser Glu Ala Thr Leu Lys
 275 280 285
 Thr Gly Gln His Leu Leu Gln Gln Gly Leu Asn Val Phe Val Ile Gln
 290 295 300
 Leu Pro Ser Gly Met Asp Pro Asp Glu Tyr Ile Gly Lys Tyr Gly Asn
 305 310 315 320
 Asp Ala Phe Thr Thr Phe Val Lys Asn Asp Lys Lys Ser Phe Ala His
 325 330 335
 Tyr Lys Val Ser Ile Leu Lys Asp Glu Ile Ala His Asn Asp Leu Ser
 340 345 350
 Tyr Glu Arg Tyr Leu Lys Glu Leu Ser His Asp Ile Ser Leu Met Lys
 355 360 365
 Ser Ser Ile Leu Gln Gln Lys Ala Ile Asn Asp Val Ala Pro Phe Phe
 370 375 380
 Asn Val Ser Pro Glu Gln Leu Ala Asn Glu Ile Gln Phe Asn Gln Ala
 385 390 395 400
 Pro Ala Asn Tyr Tyr Pro Glu Asp Glu Tyr Gly Gly Tyr Asp Glu Tyr
 405 410 415
 Gly Gly Tyr Ile Glu Pro Glu Pro Ile Gly Met Ala Gln Phe Asp Asn
 420 425 430
 Leu Ser Arg Arg Glu Lys Ala Glu Arg Ala Phe Leu Lys His Leu Met
 435 440 445
 Arg Asp Lys Asp Thr Phe Leu Asn Tyr Tyr Glu Ser Val Asp Lys Asp
 450 455 460
 Asn Phe Thr Asn Gln His Phe Lys Tyr Val Phe Glu Val Leu His Asp
 465 470 475 480

Phe Tyr Ala Glu Asn Asp Gln Tyr Asn Ile Ser Asp Ala Val Gln Tyr
485 490 495

Val Asn Ser Asn Glu Leu Arg Glu Thr Leu Ile Ser Leu Glu Gln Tyr
500 505 510

Asn Leu Asn Gly Glu Pro Tyr Glu Asn Glu Ile Asp Asp Tyr Val Asn
515 520 525

Val Ile Asn Glu Lys Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys
530 535 540

Leu Arg Glu Ala Thr Arg Ile Gly Asp Val Glu Leu Gln Lys Tyr Tyr
545 550 555 560

Leu Gln Gln Ile Val Ala Lys Asn Lys Glu Arg Met
565 570

<210> 40

<211> 597

<212> PRT

<213> *Geobacillus stearothermophilus*

<400> 40

Met Gly His Arg Ile Pro Glu Glu Thr Ile Glu Ala Ile Arg Arg Gly
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Val Asp Ile Val Asp Val Ile Gly Glu Tyr Val Gln Leu Lys Arg Gln
20 25 30

Gly Arg Asn Tyr Phe Gly Leu Cys Pro Phe His Gly Glu Lys Thr Pro
35 40 45

Ser Phe Ser Val Ser Pro Glu Lys Gln Ile Phe His Cys Phe Gly Cys
50 55 60

Gly Ala Gly Gly Asn Ala Phe Thr Phe Leu Met Asp Ile Glu Gly Ile
65 70 75 80

Pro Phe Val Glu Ala Ala Lys Arg Leu Ala Ala Lys Ala Gly Val Asp
85 90 95

Leu Ser Val Tyr Glu Leu Asp Val Arg Gly Arg Asp Asp Gly Gln Thr
100 105 110

Asp Glu Ala Lys Ala Met Thr Glu Ala His Ala Leu Leu Lys Arg Phe
115 120 125

Tyr His His Leu Leu Val His Thr Lys Glu Gly Gln Ala Ala Leu Asp
130 135 140

Tyr Leu Gln Ala Arg Gly Trp Thr Lys Glu Thr Ile Asp Arg Phe Glu
145 150 155 160

Ile Gly Tyr Ala Pro Asp Ala Pro Asp Ala Ala Lys Leu Leu Glu
165 170 175

Ser His Ser Phe Ser Leu Pro Val Met Glu Lys Ala Gly Leu Leu Thr
 180 185 190
 Lys Lys Glu Asp Gly Arg Tyr Val Gly Arg Phe Arg Asn Arg Ile Met
 195 200 205
 Phe Pro Ile His Asp His Arg Gly Glu Thr Val Gly Phe Ser Gly Arg
 210 215 220
 Leu Leu Gly Glu Gly His Pro Lys Tyr Val Asn Ser Pro Glu Thr Pro
 225 230 235 240
 Val Phe Arg Lys Gly Ala Ile Leu Tyr His Phe His Ala Ala Arg Val
 245 250 255
 Pro Ile Arg Lys Arg Gln Glu Ala Leu Leu Val Glu Gly Phe Ala Asp
 260 265 270
 Val Ile Ser Ala Ala Gln Ala Gly Ile Asp Tyr Ala Ile Ala Thr Met
 275 280 285
 Gly Thr Ser Leu Thr Glu Glu Gln Ala Arg Ile Leu Arg Pro Cys Asp
 290 295 300
 Thr Ile Thr Ile Cys Tyr Asp Gly Asp Arg Ala Gly Ile Glu Ala Ala
 305 310 315 320
 Trp Ala Ala Ala Glu Gln Leu Ser Ala Leu Gly Cys Arg Val Lys Val
 325 330 335
 Ala Ser Leu Pro Asn Gly Leu Asp Pro Asp Glu Tyr Ile Arg Val Tyr
 340 345 350
 Gly Gly Glu Arg Phe Ala Gly Glu Ala Gly Cys Arg Arg Pro Leu Val
 355 360 365
 Ala Phe Lys Met Ala Tyr Leu Arg Arg Gly Lys Asn Leu Gln His Glu
 370 375 380
 Gly Glu Arg Leu Arg Tyr Ile Asp Glu Ala Leu Arg Glu Ile Gly Lys
 385 390 395 400
 Leu Ser Ser Pro Val Glu Gln Asp Tyr Tyr Leu Arg Gln Leu Ala Glu
 405 410 415
 Glu Phe Ser Leu Ser Leu Ser Ala Leu His Glu Gln Leu Ser Arg Ser
 420 425 430
 Gln Arg Glu Arg Thr Lys Pro Arg Glu Ala Pro Asp Gly Glu Thr Ala
 435 440 445
 Arg Pro Met Leu Ala Lys Lys Leu Leu Pro Ala Phe Gln Asn Ala Glu
 450 455 460
 Arg Leu Leu Leu Ala His Met Met Arg Ser Arg Asp Val Ala Leu Val
 465 470 475 480

Val Gln Glu Arg Ile Gly Gly Arg Phe Asn Ile Glu Glu His Arg Ala
 485 490 495

Leu Ala Ala Tyr Ile Tyr Ala Phe Tyr Glu Glu Gly His Glu Ala Asp
 500 505 510

Pro Gly Ala Leu Ile Ser Arg Ile Pro Gly Glu Leu Gln Pro Leu Ala
 515 520 525

Ser Asp Val Ser Leu Leu Leu Ile Ala Asp Asp Val Ser Glu Gln Glu
 530 535 540

Leu Glu Asp Tyr Ile Arg His Val Leu Asn Arg Pro Lys Trp Leu Met
 545 550 555 560

Leu Lys Val Lys Glu Gln Glu Lys Thr Glu Ala Glu Arg Arg Lys Asp
 565 570 575

Phe Leu Thr Ala Ala Arg Ile Ala Lys Glu Met Ile Glu Met Lys Lys
 580 585 590

Met Leu Ser Ser Ser
 595

<210> 41

<211> 603

<212> PRT

<213> Bacillus subtilis

<400> 41

Met Gly Asn Arg Ile Pro Asp Glu Ile Val Asp Gln Val Gln Lys Ser
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Ala Asp Ile Val Glu Val Ile Gly Asp Tyr Val Gln Leu Lys Lys Gln
 20 25 30

Gly Arg Asn Tyr Phe Gly Leu Cys Pro Phe His Gly Glu Ser Thr Pro
 35 40 45

Ser Phe Ser Val Ser Pro Asp Lys Gln Ile Phe His Cys Phe Gly Cys
 50 55 60

Gly Ala Gly Gly Asn Val Phe Ser Phe Leu Arg Gln Met Glu Gly Tyr
 65 70 75 80

Ser Phe Ala Glu Ser Val Ser His Leu Ala Asp Lys Tyr Gln Ile Asp
 85 90 95

Phe Pro Asp Asp Ile Thr Val His Ser Gly Ala Arg Pro Glu Ser Ser
 100 105 110

Gly Glu Gln Lys Met Ala Glu Ala His Glu Leu Leu Lys Lys Phe Tyr
 115 120 125

His His Leu Leu Ile Asn Thr Lys Glu Gly Gln Glu Ala Leu Asp Tyr
 130 135 140

Leu Leu Ser Arg Gly Phe Thr Lys Glu Leu Ile Asn Glu Phe Gln Ile
 145 150 155 160
 Gly Tyr Ala Leu Asp Ser Trp Asp Phe Ile Thr Lys Phe Leu Val Lys
 165 170 175
 Arg Gly Phe Ser Glu Ala Gln Met Glu Lys Ala Gly Leu Leu Ile Arg
 180 185 190
 Arg Glu Asp Gly Ser Gly Tyr Phe Asp Arg Phe Arg Asn Arg Val Met
 195 200 205
 Phe Pro Ile His Asp His His Gly Ala Val Val Ala Phe Ser Gly Arg
 210 215 220
 Ala Leu Gly Ser Gln Gln Pro Lys Tyr Met Asn Ser Pro Glu Thr Pro
 225 230 235 240
 Leu Phe His Lys Ser Lys Leu Leu Tyr Asn Phe Tyr Lys Ala Arg Leu
 245 250 255
 His Ile Arg Lys Gln Glu Arg Ala Val Leu Phe Glu Gly Phe Ala Asp
 260 265 270
 Val Tyr Thr Ala Val Ser Ser Asp Val Lys Glu Ser Ile Ala Thr Met
 275 280 285
 Gly Thr Ser Leu Thr Asp Asp His Val Lys Ile Leu Arg Arg Asn Val
 290 295 300
 Glu Glu Ile Ile Leu Cys Tyr Asp Ser Asp Lys Ala Gly Tyr Glu Ala
 305 310 315 320
 Thr Leu Lys Ala Ser Glu Leu Leu Gln Lys Lys Gly Cys Lys Val Arg
 325 330 335
 Val Ala Met Ile Pro Asp Gly Leu Asp Pro Asp Asp Tyr Ile Lys Lys
 340 345 350
 Phe Gly Gly Glu Lys Phe Lys Asn Asp Ile Ile Asp Ala Ser Val Thr
 355 360 365
 Val Met Ala Phe Lys Met Gln Tyr Phe Arg Lys Gly Lys Asn Leu Ser
 370 375 380
 Asp Glu Gly Asp Arg Leu Ala Tyr Ile Lys Asp Val Leu Lys Glu Ile
 385 390 395 400
 Ser Thr Leu Ser Gly Ser Leu Glu Gln Glu Val Tyr Val Lys Gln Leu
 405 410 415
 Ala Ser Glu Phe Ser Leu Ser Gln Glu Ser Leu Thr Glu Gln Leu Ser
 420 425 430
 Val Phe Ser Lys Gln Asn Lys Pro Ala Asp Asn Ser Gly Glu Thr Lys
 435 440 445

Thr Arg Arg Ala His Leu Thr Thr Lys Ala Arg Gln Lys Arg Leu Arg
 450 455 460
 Pro Ala Tyr Glu Asn Ala Glu Arg Leu Leu Leu Ala His Met Leu Arg
 465 470 475 480
 Asp Arg Ser Val Ile Lys Lys Val Ile Asp Arg Val Gly Phe Gln Phe
 485 490 495
 Asn Ile Asp Glu His Arg Ala Leu Ala Ala Tyr Leu Tyr Ala Phe Tyr
 500 505 510
 Glu Glu Gly Ala Glu Leu Thr Pro Gln His Leu Met Ala Arg Val Thr
 515 520 525
 Asp Asp His Ile Ser Gln Leu Leu Ser Asp Ile Leu Met Leu Gln Val
 530 535 540
 Asn Gln Glu Leu Ser Glu Ala Glu Leu Ser Asp Tyr Val Lys Lys Val
 545 550 555 560
 Leu Asn Gln Arg Asn Trp Ser Met Ile Lys Glu Lys Glu Ala Glu Arg
 565 570 575
 Ala Glu Ala Glu Arg Gln Lys Asp Phe Leu Arg Ala Ala Ser Leu Ala
 580 585 590
 Gln Glu Ile Val Thr Leu Asn Arg Ser Leu Lys
 595 600